



08/984079

CTT TCT ATT TGG TTA ACC ATG GCT CAT AAC TTT CGT CAT CCT TTC TTC
Leu Ser Ile Trp Leu Thr Met Ala His Asn Phe Arg His Pro Phe Phe>
20 40
CTT TTC CAA CTT TTA CTC ATT ACT GTC TCA CTA ATG ATC GGT AGC CAC
Leu Phe Gln Leu Leu Ile Thr Val Ser Leu Met Ile Gly Ser His>
60 80
100 120 140
ACC GTC TCG TCA GCG GCT CGA CAT TTA TTC CAC ACA CAA ACC ACC TCA
Thr Val Ser Ser Ala Ala Arg His Leu Phe His Thr Gln Thr Thr Ser>
160 180
TCA GAG CTG CCA CAA TTG GCT TCA AAA TAC GAA AAG CAC GAA GAG TCT
Ser Glu Leu Pro Gln Leu Ala Ser Lys Tyr Glu Lys His Glu Glu Ser>
200 220 240
GAA TAC AAA CAG CCA AAA TAT CAT GAA GAG TAC CCA AAA CAT GAG AAG
Glu Tyr Lys Gln Pro Lys Tyr His Glu Glu Tyr Pro Lys His Glu Lys>
260 280
CCT GAA ATG TAC AAG GAG GAA AAA CAA AAA CCC TGC AAA CAT CAT GAA
Pro Glu Met Tyr Lys Glu Glu Lys Gln Lys Pro Cys Lys His His Glu>
300 320
GAG TAC CAC GAG TCA CGC GAA TCG AAG GAG CAC GAA GAG TAC GAT AAA
Glu Tyr His Glu Ser Arg Glu Ser Lys Glu His Glu Glu Tyr Asp Lys>

FIGURE 1A



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340
GAA AAA CCC GAT TTC CCC AAA TGG GAA AAG CCT AAA GAG CAC GAG AAA
Glu Lys Pro Asp Phe Pro Lys Trp Glu Lys Pro Lys Glu His Glu Lys>
360
400
CAC GAA GTC GAA TAT CCG AAA ATA CCC GAG TAC AAG GAG CAC AAA CAA GAT
His Glu Val Glu Tyr Pro Lys Ile Pro Glu Tyr Lys Asp Lys Gln Asp>
440
GAG AAT AAG AAA CAT AAA GAT GAA GAG TGC CAG GAG TCA CAC GAA TCG
Glu Asn Lys Lys His Lys Asp Glu Glu Cys Gln Glu Ser His Glu Ser>
460
500
AAA GAG CAC GAA GAG TAC GAG AAA GAA AAA CCC GAT TTC CCC AAA TGG
Lys Glu His Glu Glu Tyr Glu Lys Glu Lys Pro Asp Phe Pro Lys Trp>
540
GAA AAG CCT AAA GGG CAC GAG AAA CAT AAA GCC GAA TAT CCG AAA ATA
Glu Lys Pro Lys Gly His Glu Lys Glu Lys His Lys Ala Glu Tyr Pro Lys Ile>
580
600
CCT GAG TGC AAG GAA AAA CTA GAT GAG GAT AAG GAA CAT AAA CAT GAG
Pro Glu Cys Lys Glu Lys Leu Asp Glu Asp Lys Glu His Lys His Glu>
620
640
TTC CCA AAG CAT GAA AAA GAA GAG GAG AAG AAA CCT GAG AAA GGC ATA
Phe Pro Lys His Glu Lys Glu Glu Lys Lys Pro Glu Lys Gly Ile>
660

FIGURE 1B



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680 720
GTA CCC TGA GTG GGT TAA AAT GCC TGA ATG GCC GAA GTC CAT GTT TAC
Val Pro *** Val Gly *** Asn Ala *** Met Ala Glu Val His Val Tyr>
740 760
TCA GTC TGG CTC GAG CAC TAA GCC TTA AGC CAT ATG ACA CTG GTG CAT
Ser Val Trp Leu Glu His *** Ala Leu Ser His Met Thr Leu Val His>
780 800
GTG CCA TCA TCA TGC AGT AAT TTC ATG GGA TAT TGT AAT TAT ATT GTT
Val Pro Ser Ser Cys Ser Asn Phe Met Gly Tyr Cys Asn Tyr Ile Val>
820 840 860
AAT AAA AAA GAT GGT GAG TGG GAA ATG TGT GTG TGC ATT CAT CCA TGA
Asn Lys Lys Asp Gly Glu Trp Glu Met Cys Val Cys Ile His Pro ***>
880 900
GCA ATG CTG AAT CTC TTT GCA TGC ATA GAG ATT CTG AAT GGT TAT AGT
Ala Met Leu Asn Leu Phe Ala Cys Ile Glu Ile Leu Asn Gly Tyr Ser>
920 940 960
TTA TGT TAT ATC GTT TGT TCT AGT GAA ATT AAT TTT GAA TGT TGT ATG
Leu Cys Tyr Ile Val Cys Ser Ser Glu Ile Asn Phe Glu Cys Cys Met>
TAA TGT T
*** Cys Xxx>

FIGURE 1C



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20 40 60
ACTAAAGGGA ACAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT
80 100 120
CCCCCGTGGA CTAACAACAAA CATGGGAAGA TTTGCTGTAA AAAAAATAAAA GAAGCTTACT
140 160 180
CAATAACACT TTGTGAATTG TATACAAAAG ACTCAATGAA AAACAATAAC TCAATACACT
200 220 240
TTTTTTCAC TATTACATC CTTTATATAG GCTGAAACTA CAACAACCTT AGCTAAAAAA
260 280 300
ATAGGATAAC CTAATAGCAA AATCACAATC AGATATTAAA CCATGATTTT AGCTAACCAT
320 340 360
TTAACAACTT TATTGAAACT AATTGAATA TTTTCATCTGC TGATATGCCC AAGATTTTAG
380 400 420
GCCACTAACC GATTGGTGG TGAACCTTAA CATGTCATGC ATTTGTAACT GTTTGAAACA
440 460 480
AGTTTTTTTGC ATTATTTTAC TATATGAACT GTTTGATTAG GTTGAGTTAC ACACTGAGCT
500 520 540
TGTAAGCTCA CTCAAAATTTT TCCTAATTCT AAGGTGATCA GCAAACCTAG GACCGGGCGG
560 580 600
CGTACGAGAG CTCGGATTGA TTTTCTAGTT AATAAATAAG ACGATTATG TTTTAACT

Figure 2A



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620	ATTATGGACT TTTTGGACTA TGTAAGTGT TGGGACTTTA TTTTGTGTTT TTATTTGCTT	640	660
680	TTTTTGGATT TAGTAATTAT TATTTTAAA CTGCAAAATT ATATGTTTTT ACAAACTAAG	700 *	720
740	TCACAGTTTT CAAAATTCCA TAACTTAGAA TTTTTCGCTG CAAAATAAAG TAATCATTTA	760	780
800 *	AGTGTTTTTT CTGTAATAAA ATAAATAAAT AATTTTAAAG AGTATTTTCC TAAAAATTGG	820	840
860	AAATTGATTT ACCAAAATTA GTATGTCAAA ACACATGTTT ATATGTTACA GGGCGATATC	880	900 *
920	GTCTAGGCAA ATAACATCTA GCGGGGGTTT GGAGTGTAC AGGGCGAGTG GGCTCATTTT	940	960
980	GAGTAAGTAT AGTTAGGCC GAGTTTAGA TTGCATATTC AAGGTCAAAG ATTTTGTAAG	1000 *	1020
1040	CTTCGATGAA TGATATGTAT GATTGTCCGA TTAACGAAAT ATGTTTTTTT CTTTTGTGTG	1060	1080
1100 *	TGTTTTATCT CGTGTGATAA GTATATAGTA TGTTTTATTC CAATCTTAT GGCATGTGAC	1120	1140
1160	ATTGTGGCTA TTCTAATTAA ATTGATTGT TATTATTGAA ATCTGATGCA TCTGTCTTAC	1180	1200 *

Figur 2B



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1220	AAAGCATGGA ATCTCATGCC TACTGCTTTC TGTTAAAGAT ACGATTGCAA GTTTAACATG	1240	1260
1280	CTTACTATTT TGATTTTGTC CTTGCAATGCT ATGTCACATT ACATGGGGTT GGGATGATAT	1300 *	1320
1340	GGTAAGGAGG AAGTTTGGAC AGTTTAATGA TTTGCACTAT CTGGTGGTTT AACACATAT	1360	1380
1400 *	TTGTTATGGC ATCTTGACTG CCGTTATGGT GGCTCGACCG CCCATATCTG TTCTGGAAAT	1420	1440
1460	TTATCTGTGA CTCGTGGTGC ATTGTCTACA ATTATTTGTT GGTGTGTTTT GGATGGACGA	1480	1500 *
1520	GTCGTGGGA ACTCTATTG GTGTGTGCG GAGTTGGTA GGAAATTTTC GAAAAAAT	1540	1560
1580	TGCATTGTGT TTTTCTGAAA AATATTGCAT TAACATAATC ATGCATCTC AATTTTGGTC	1600 *	1620
1640	AATTGAACGT TATAAAATTC TCTATGATAT CCTGATCTGT TTATTACATT ATATGTGTTT	1660	1680
1700 *	ATGCTTGAGT TAAAGTCAAAC ATTGAGATTC ATAGCTCACC CAATTATTTA ATCATTTTCAG	1720	1740
1760	GCAATCTGCA GACTTAGGAT TGGATGGCGT TCAGGAGCTT GGATTGGTTT TCTCACATCA	1780	1800 *
1820	TATTTTATTA AATAATTATT AATTAAAATT TATGGACTTT TGGACTGTCT GACTAAATTTT	1840	1860

Figure 2C



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20 40 60
ACTAAAGGGA ACAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGG ATCCCCCGTG
80 100 120
GACTAAACAA AACATGGGAA GATTGCTGT AAAAAAATAA AAGAAGCTTA CTCAATAACA
140 160 180
CTTTGTGAAT TGTATACAAA AGACTCAATG AAAACAATA ACTCAATACA CTTTTTTTCA
200 220 240
CTGATTTACA TCCTTTATAT AGGCTGAAAC TACAACAAC TTAGCTAAAA AAATAGGATA
260 280 300
ACCTAATAGC AAAATCACAA TCAGATATTA AACCATGATT TTAGCTAACC ATTTAACAAC
320 340 360
TTTATTGAAA CTAATTGAA TATTTCATCT GCTGATATGC CCAAGATTTT AGGCCACTAA
380 400 420
CCGATTGGT GGTGAACTTT AACATGTCTAT GCATTGTAA CTGTTTGAAA CAAGTTTTTT
440 460 480
GCATTATTTT ACTATATGAA CTGTTTGATT AGGTTGAGTT ACACACTGAG CTTGTAAGCT
500 520 540
CACTCAAATT TTTCTAATTT CTAAGGTGAT CAGCAAACCT AGGACCGGGC GCGGTACGAG

Figure 3A



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560	AGCTCGGATT GATTTTCTAG TTAATAAATA AGACGATTTA TGTTTTTAAA CTATTATGGA	580	600 *
620	CTTTTGGAC TATGTAAC TG TTTGGGACTT TATTTTGTG TTTTATTGTC TTTTTTTGGA	640	660
680	TTTAGTAATT ATTATTTTAA AACTGC AAAA TTATATGTTT TTACAAAATA AGTCACAGTT	700 *	720
740	TTCAAAATTC CATAACTTAG AATTTTTCGC TGCAAAAATA AGTAATCATT TAAGTGTTTT	760	780
800 *	TTCTGTAATA AAATAAATAA ATAATTTTAA CGAGTATTTT CCTAAAAATT GGAAATTGAT	820	840
860	TTACCAAAAT TAGTATGTCA AAACACAATGT TTATATGTTA CAGGGCGATA TCGTCTAGGC	880	900 *
920	AAATAACATC TAGGCGGGT TTGGAGTGTT ACAGGGCGAG TGGGCTCATT TTGAGTAAGT	940	960
980	ATAGTTAGGG CCGAGTTTAA GATTGCATAT TCAAGGTCAA AGATTTTGTA AACTTCGATG	1000 *	1020
1040	AATGATATGT ATGATTGTCC GATTAACGAA ATATGTTTTT TTCTTTTGTG TGTGTTTTAT	1060	1080



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1100 *	1120	1140
CTCGTGTGAT AAGTATATAG TATGTTTTAT TCCAATTCTT ATGGCATGTG ACATTGTGGC		
1160	1180	1200 *
TATTCTAATT AAATTGATTT GTTATTATTG AAATCTGATG CATCTGTTCT ACAAAAGCATG		
1220	1240	1260
GAATCTCATG CCTACTGCCTT TCCTGTTAAAG ATACGATTGC AAGTTTAAACA TGCTTACTAT		
1280	1300 *	1320
TTTGATTTTG TCCTTGCATG CTATGTCACA TTACATGGGG TTGGGATGAT ATGGTAAAGGA		
1340	1360	1380
GGAAGTTTIG ACAGTTTAAAT GATTGCACT ATCTGGTGGT TTAACCACAT ATTTGTTATG		
1400 *	1420	1440
GCATCTTGAC TCGGGTTATG GTGGCTCGAC CGCCCATATC TGTTCTGGAA ATTTATCTGT		
1460	1480	1500 *
GACTCTGGTG GCATTGTCTA CAATTATTG TTGGTGTGTT TTGGATGGAC GAGTCGTGGG		
1520	1540	1560
GAACTCTATT TGGTGTGTTG CGGAGTTGGG TAGGAAATTT TCGAAAAAAA TTTGCATTGT		
1580	1600 *	1620
GTTTTTCTGA AAAATATTGC ATTAACATAA TCATGCATTC TCAATTTTGG TCAATTGAAC		

Figure 3C



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1640 1660 1680
GTTATAAAAT TCTCTATGAT ATCCTGATCT GTTTATTACA TTATATGTGT TTATGCTTGA
1700 * 1720 1740
GTTAAGTCAA ACATTGAGAT TCATAGCTCA CCCAATTATT TAATCATTTT AGGCAATCTG
1760 1780 1800 *
CAGACTTAGG ATTGGAATGGC GTTCAGGAGC TTGGATTGGT TTCTCTCACAT CATATTTTAT
1820 1840 1860
TAAATAAATTA TTAATTAAAA TTTATGGACT TTTGGACTGT CTGACTAATT TTCAGAAATTT
1880 1900 * 1920
TATTTTGGTT TTGGGTTTTG TTGAATTTTT TAGATAAATTA TTTTAAATAT TCTGCATAAT
1940 1960 1980
TTTTCTGTTA TTTGAAAAGG ATGTTGGAAT TTTTTTTTCAA AATTGAAACG TTTAAGAATT
2000 * 2020 2040
TTTACTACTG CAAATTCAGA ATAAGTGAAT TTGTTTTTTTA GAAAGATTAA ATAAGTTAGT
2060 2080 2100 *
ATTACGATTT TTAGTTTGAT TTGGTGGAAG GTAATGTATG TTTTGAACA TAATTATTG
2120 2140 2160
ACAATAATTA AGTTTCTTAG GGAATAAAG GAAATATCTT CTCTTTTTTT GTAAATAC

Figure 3D



Figure 3E



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2720 2740 2760
AACCAAAATGA CACAAATTTC ATGATTAGTT AGATCAAGCT TTGAGTCTTT CAAAACATAA
2780 2800 2820
AAATTACAAA AAAAAACAA ACTTAAATC ATTTATCAAT TTGAACAACA AAGCTTGGCC
2840 2860 2880
GAATGCTAAG AGCTTAAAAA TGGCTTCTTT TGTTCCTTTT TGTTGCAAC GGTGGAGAGA
2900 2920 2940
AGAGGGAAT GAAGATTGAC CATATTTTTT TATTATGTTT TAACATATAA TATTAATAAT
2960 2980 3000
TTAATCATAA TTATACTTTG GTGAATGTGA CAGTGGGAG ATACGTAAAG TATTTTAACA
3020 3040 3060
TTATACTTTT TGCAAGCAGT TGGCTGGTCT ACCCAAGAGT GATCAAAGTT TGAGCTGCCT
3080 3100 3120
TCAATGAGCC AATTTTGGC CATAATGGAT AAAGGCAATT TGTTTAGTTC AACTGCTCAC
3140 3160 3180
AGAATAATGT TAAATGAAA TTAAAAAAG GTGGCCTGGT CACACACACA AAAAAAACT
3200 3220 3240
AATGTTGGTT GGTGAATTT TATATTACGG AATGTAATAT TATATTTTAA AATAAAATTA

Figure 3F



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3260	3280	3300 *
TGTTATTTAG ATTCTTAATA TTTTGGAGCA TTCCATACTA TAATTTTCGTA ACATAATATT		
3320	3340	3360
AAAATATAGT AATATAAAGT GTAATTAACT TTAAATTACA AGCATAATAT TAAATTTTGA		
3380	3400 *	3420
ATCAATTAAT TTTTATTCTTCT ATTATTTTAA TTAATTTAGT CTATTTTTC AAAATAAAAT		
3440	3460	3480
TTAAATCTAA ATAAAAATAA TTTTTCCTTA ATGTTGAAAC AACTCATGTT ATACTTCAAA		
3500 *	3520	3540
ATTATAAGTA TTATATTTAC CTTGATGATT TATTTATTAG TATATTAATT CTGATTATAA		
3560	3580	3600 *
TTATGGTGG ATACAAATCGC TTTCCACTAA ATATTTTAACT TATGATTAT AAATTTATT		
3620	3640	3660
CAACATCGTA TATTTACTTA TTAATACATA ATTTATCATA ATTTTATGGA AATTGAGACC		
3680	3700 *	3720
AAGAAACATT AAGAGAACAA ATTCATAAC AAAGACAATT TAGAAAAAAA TGTACTTTTA		
3740	3760	3780
GGTAATTTTA AGTACTCTTA ACCAAACACA AAAATTCAAA TCAAATGAAC TAAATAAGAT		



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3800 * 3820 3840
AATATAACAT ACGGAACATC TTAAGTTGTA TCTTACATTC CCATAATTTT ATTATGAAAA
3860 3880 3900 *
ATAATCTTAT ATTACTCGAA CTAAGTTGTTG TCACAAATTA TTATCTAAAT AAAGAAAAAC
3920 3940 3960
ACTTAATTTT TATAACATTT TTTTCATATAT TTGAAAGATT ATATTTTGTG TATTTACGTA
3980 4000 * 4020
AAAAATATTG ACATAGATTG AGCACCTTCT TAACATAATC CCACCATAAG TCAAGTATGT
4040 4060 4080
AGATGAGAAA TTGGTACAAA CAACGTGGGG CCAATCCCA CCAAAACCATC TCTCATCTC
4100 * 4120
TCCATATAAA GGCTTGCTAC ACATAGACAA CAATCCACAC A CA AAT ACA CGT TCT
4140 4160 4180
TTT CTT TCT ATT TGA TTA ACC ATG G CTCATAGCAT TCGTCACCCCT TTCTTCCTTT
<Lys Lys Arg Asn Ser *** Gly His
<Ile Cys Thr Arg
4200 * 4220 4240
TCCAACTTTT ACTCATAAGT GTCTCACTAG TGACCCGGTAG CCACACTGTT TCGGCAGCGG
4260 4280 4300 *
CTCGACGTTT ATTCGAGACA CAAGCAACCT CATCAGAGCT CCCACAATTG GCTTCAAAAT

Figure 3H



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4320	ACGAAAAGCA	CGAAGAGTCT	GAATACGAAA	AGCCAGAATA	CAAAACAGCCA	AAGTATCACG
						4360
4380						
						4420
						4480
						4540
						4600
						4660
						4720
						4780
						4840
						4900
						4960
						5020
						5080
						5140
						5200
						5260
						5320
						5380
						5440
						5500
						5560
						5620
						5680
						5740
						5800
						5860
						5920
						5980
						6040
						6100
						6160
						6220
						6280
						6340
						6400
						6460
						6520
						6580
						6640
						6700
						6760
						6820
						6880
						6940
						7000
						7060
						7120
						7180
						7240
						7300
						7360
						7420
						7480
						7540
						7600
						7660
						7720
						7780
						7840
						7900
						7960
						8020
						8080
						8140
						8200
						8260
						8320
						8380
						8440
						8500
						8560
						8620
						8680
						8740
						8800
						8860
						8920
						8980
						9040
						9100
						9160
						9220
						9280
						9340
						9400
						9460
						9520
						9580
						9640
						9700
						9760
						9820
						9880
						9940
						10000

Figure 3I



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4920	4940	4960
TTACAAAGTTA AGACATGTAT AAATATATGA CAATATAAATT ACAAGTTTTTA GTTCAATGTTT		
4980	5000 *	5020
AGCTATCTTA GATGTTTATT GATGATCTTA ATTACATTTA AACAAATTCC ACTTAAAAATT		
5040	5060	5080
TTAATAAATA ATAACAAATA ATTATTGTAA TATAATACAT TAAATGCAAC AAAAAATGAA		
5100 *	5120	5140
ATAAATAAAA TAAATAGCA AATAATTGTT ATAATATTGT AATATAATAT GTACCATATT		
5160	5180	5200 *
CTTAACTGAA ATAGGGTCTA ACCTATAATC CCTAAAATTT CAGTTTAAAT ATTTTATATAC		
5220	5240	5260
CTGCCATATT ATTAGAACTC TTTTAAATA TATTAAAATT TTAATTATAC CAATTTAATT		
5280	5300 *	5320
TAAACTATTA ATTATCTTAA CTAATACTA AAATTTTATT TAACCTATTA ATTAAATTCC		
5340	5360	5380
TAATTATCTT ATCTAATTTA AAACCTCTAAT TATCCCTAATT TGATTTAAAT TCTTGATTAT		
5400 *	5420	5440
CTTAATTGTT AACCTCCTCC ACCCAGCTAG ATGCTGGACC CGAATCCGGG AGATTACATC		



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5460 5480 5500 *
GGCATTGAGA TGGCCTAGTA GTGATCAGGG TTTTCTAGAG GTACCCAATT CGCCCTATAG

TGAGTCGT



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AAAAAACA ATG AGC ACT GCA AGA TTT ATC AAG TGT GTC ACG GTC GGT GAT 50
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
1 5 10
GGA GCT GTG GGG AAA ACT TGT ATG CTC ATT TCA TAT ACC AGC AAT ACT 98
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
15 20 25 30
TTC CCA ACG GAT TAT GTT CCA ACA GTA TTT GAT AAC TTT AGT GCC AAT 146
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
35 40 45
GTG GTG GTG GAT GGC AGC ACA GTG AAC CTT GGC CTA TGG GAC ACT GCC 194
Val Val Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
50 55 60
GGG CAA GAA GAT TAT AAT AGG CTA AGG CCA CTG AGT TAT AGA GGA GCT 242
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
65 70 75
GAT GTG TTT TTG TTG GCC TTT TCT CTT ATA AGC AAG GCC AGT TAT GAA 290
Asp Val Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
80 85 90
AAC ATC TAC AAA AAG TGG ATC CCA GAG CTA AGA CAT TAT GCT CAT AAT 338
Asn Ile Tyr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala His Asn
95 100 105 110
GTA CCA GTT GTG CTT GTT GGA ACC AAA CTA GAT TTG CGA GAT GAC AAG 386
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Lys
115 120 125
CAG TTC CTC ATT GAT CAC CCT GGA GCA ACA CCA ATA TCA ACA TCT CAG 434
Gln Phe Leu Ile Asp His Pro Gly Ala Thr Pro Ile Ser Thr Ser Gln
130 135 140

FIGURE 4A



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GGG GAA GAA CTA AAG AAG ATG ATA GGA GCA GTT ACT TAT ATA GAA TGC 482
Gly Glu Glu Leu Lys Lys Met Ile Gly Ala Val Thr Tyr Ile Glu Cys
145 150 155

AGC TCC AAA ACC CAA CAG AAT GTG AAG GCT GTT TTC GAT GCT GCA ATA 530
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
160 165 170

AAA GTA GCT TTG AGG CCA CCA AAA CCA AAG AGA AAG CCT TGC AAA AGG 578
Lys Val Ala Leu Arg Pro Pro Lys Pro Lys Arg Lys Pro Cys Lys Arg
175 180 185 190

AGA ACA TGT GCT TTC CTT TGAATATGG ATCATTTATTA CAGTCAAAAA 626
Arg Thr Cys Ala Phe Leu
195

CAGTTAACAA AAGCTGTTGC AGATAAACAC TGAATCTGCT ATAGTTTGTT TTGTTTAC 686

ATATGTTCCA CGTGAAACTA TGAAGCATCT CTAAGAAAAAC CCAAACTATC ATATCAACCC 746

ATCGATCAAT GAATCGATTT CAATTTTCGC AGTATAAGTT CCTTTTAATC CTTTCTTTT 806

ACTTCATTTT ATAACGAATT CTATGGATAA TGTTCCCTAC AAACATGTCA TTACAATGTT 866

TAATTATAAA TTCCATTCTT CTATTTTACT AAAAAAAAAA AAAA 910

FIGURE 4B



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20 40 60
TTGGATGAGA ACCAATTTT AATAGTAAAN CCTAACCAAT TTTTAATAAT AAAGCTGACT
80 100 120
CCTAGTACAA GAGCTTTTAT TCATTCTTCT ATTTTGCTTT CCTCTAGGCT TGGCAATCGA
140 160 180
GAATTTTCTT GTGTTACAAT ATAATAAATA CATCGTAGAA ATAAATTTTA TTCAAAATTGA
200 220 240
AGTCTTAACC ATCTTTAATA TTTGTAGATG TAATTTAAAT GAAAGATAAA TACATATTCT
260 280 300
TGGACATGTA TTTTCATCTT AATGTTTGTG GCTTTGGTGA TAGGTGTATT GATGTACGAT
320 340 360
GTCTTTTAAA TCACATATCA CATTITGAGT TTGTATGATG ATAAGTCGAC ATAANCGAAA
380 400 420
TATGGTGTGA TCTTCACITT TGAACITTGA TAAGTCACCA AACTTTAACA AAGTTTGATT
440 460 480
GTGTACATAT ATATATATAT CTTCAAAATTT TATAATAAAA ATTGTGTTTA AATAATTTAC
500 520 540
AGTTATATTA TTTTTTATC TCTAATTTTA TTTGTGCGCA AATTTTGTAGT TGATATTTTA
560 580 600
ACATAAAAAA AATTGTACAC ATTTACAAGC CCATATACAA ATAATTATAT AAATATTTCAT

FIGURE 5A



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TAAAAAATAT	ATTAAATAT	AGGATATAAA	TATAACTATT	TTAGAATTAT	TCTACTTTAA
620	640	660			
GATAACATAG	GTAAATGTA	TAATTAATAA	GGTTAGTTTA	TTGTAAAGAT	GAGTATATAT
680	700	720	*		
GTCGTAAACA	TAATCACTAA	CCATTTTTTAT	TAACTTCTTG	GTTTGTGAAGT	TCCAAAAAGA
740	760	780			
AAATGGAAGG	GAAATTTGAG	AGTAAGTTCA	TGTTTATATT	ATACATAATG	AAGTTGATGT
800	820	840	*		
TTTCTTCTTT	TTAATATTTT	TATACAAAAAT	ATTTAAATAA	AATAATTAAG	GATTGAATGA
860	880	900	*		
AAAAATATAAT	GAAAGTCGTT	TTACTAATAG	TCATATTGCA	TTTTGTGCGCA	TCTACTTTAAA
920	940	960			
TAATAGATAA	ATTAATTGTG	GTACATTAGA	TCAAAGAACA	AACTAGATTT	TGTCCCATTTC
980	1000	1020	*		
TATGTGTAAA	AGCTGGTCCG	TTTACATTAA	AATAAGGTAC	ATGTTACATG	CCACGTATAA
1040	1060	1080			
CTATCTGGTT	ATTCTATCAA	TCACGCTAAT	TTTTAAACAGT	AGAAAATGAAT	GTAATTTTTTA
1100	1120	1140	*		
AATAGAAAGG	GTCAAATTGT	TATTTGATCT	AACACGTAGG	GATTAAATTA	CTTATTTTCC
1160	1180	1200	*		

FIGURE 5B



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1220 TAAAGAAATA AGTAAATAT AATTGAATC TTAATACAAA AACTTTCATG ATACTTTTAT 1260
1280 CATATTTTAC TTATAATTTA ATATTGTGAG AGTAACAAAR TTAAAAAACA TAGAAACACC 1320
1340 AAAAGTTAGT TATGGTGTGA CTCATATACA CAGTTAAAAAT TTGAATAAAT TTTTTCCTTC 1380
1400 GTCATTAATT CCATCATGGG TTTTTTTTTT TCTAGTTAAG CCATAATTAT CAAAAATAATC 1440
1460 ATCATTAATC CTATCAATAC CCGGCCCTGC CTCCCTCCCT CAATACTTAA ACCCAACTAA 1500
1520 CACCCAGCAC CAAACGCACT TTAATAGCCA CCTATTCTA GCCATGTCCT TGCACCTAAA 1560
1580 GAAAAGTAA GCTAACCTGC AATCATTTCCA TATCGAGGCC TCAACAGATA AAGTTGGTTG 1620
1640 ATGGGTTTGC ACCAAGTGT TAAAACCCGG CCCTCAACTT CCCTTTTCTT TTCATCCTCC 1680
1700 CCACTCCACA CCCTCCAATT TTCTTCATAT GGTTCATTA TAAGTTCCTT ATAATCACAG 1740
1760 AATCAAGATA AGTCCTCAGC AAACAAAAA CCATGGCTCT CGAGCAAGAT CTGGACTAGT 1800

FIGURE 5C



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1820	1840	1860
CAGAGCTCTG AATATTTGGAT CATTATTACA GTCAAAAACA GTTAACAAAA GCTGTTGCAG		
1880	1900	1920
ATAAACACTG AATCTGCTAT AGTTTGTGTTT TGGTTTACAT ATGTTCCACG TGAAACTATG	*	
1940	1960	1980
AAGCATCTCT AAGAAAACCC AAACATATCAT ATCAACCCCAT CGATCAATGA ATCGATTTC		
2000	2020	2040
ATTTTCGCAG TATAAGTTCC TTTTAATCCT TTCTTTTITAC TTCATTTTAT AACGAATTCT		
2060	2080	2100
ATGGATAATG TTCCCTACAA ACATGTCATT ACAATGTTTA ATTATAAATT CCATTCTTCT		*
2120	2140	2160
ATTTTACTAA GATATTAGTA ACTTCAAACT GCTGATTTT ACTAATTTAT TATTATATAA		
2180	2200	2220
TTGTTAGAAT GATTATTTT CAATAATTTA ACAACAATAT TTAATATTAT TATTATTATT	*	
2240	2260	2280
ATTTCTCAAT TTTTATTAAA CAAAAACATA AATTTTIGAC AAATTAATAA AAATGAATTA		
2300	2320	2340
ATTTCTCAAT TTTTCGTGCA ACTATTACAA AAATCCTTCA TAGTCCTAAT CTTAATTGTA	*	
2360	2380	2400
TGCAGAGGTG ATAATAATCT TAATTGATG CAGAGGTAAT AATGGGCCGG GTTTGAGCTG		*

FIGURE 5D



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2420	2440	2460
GACTTAAGCA TGATATTGAC GTACTTTTATA TTTTTCCTAAA TTCAACCCAG CTCGAAATAT		
2480	2500 *	2520
GAGTCTAAAA TTTTGTCCAA TTTAAATCCAA GCCCATTTTA AGTTCGTCCA TATTATTTTT		
2540	2560	2580
TAATTTAAAA AATTATATC ATTTTATTTT AATATTTAAT TATTTTATAT ATTTTATTAT		
2600 *	2620	2640
TATTGAAAAAT TTTTATATAG TCATCTTAAC ATTATGTTAA TGTTTATATT AGAGTAGTAT		
2660	2680	2700 *
TATATATATT TAGTATAGGT TTATTTTGGT AATAAACTTA AAAATGGGTC TTGTGGGCTA		
2720	2740	2760
GACTTGGACC TTAAATGCTC AAACTCAAAC TTAATTCATA TTTTAAACAG GCTTAATATT		
2780	2800 *	2820
TTTATTTTACA CTGTTTCAA TTTTTCGGGT GAAATATCTT CGAGTCTAGA TTAATAACAC		
2840	2860	2880
CACAGGTCTA ATTTGATGCT CAATGAAAAAT GAAATCATAT TGAGCTTAAT TAATATTCCA		
2900 *	2920	2940
TTCTTCTTTG CTGAAAGGAC CAAGCAATTC GAGTTACATT AAGGTTAAAG AGTATGGGAT		
2960	2980	3000 *
CCGCCAAACC TGCCCCAATG TCTCTTCAAC CATCCAAAAA CTTGAGTCAG TATCACATAC		

FIGURE 5E



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3020 ATGTACCGNT ATTTATTTAT TTATTGAAAT TGGCATTATT TCTTG
3040

FIGURE 5F



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GGGCATTCCA CAGGACCATG TGTCCTCCCTAT TTCCAGGCAT TTTGAGACTT CACCTAAACT 60
TCTAGAGTTG TTTCAAATTA GCCCCTATTT GTTCTTAAAT CATTTTAGGA TCTTGTAAC 120
TCGTATTTAG GACTAAATGT GTAATTTATA CTTTAATTAT GATTGATTAA TTGATTGATT 180
TNGTAGTAAT GCCCGTGACC CTAATCCGTT AGCGAAGAGG GGTAGGGGT TAGGGGTTTT 240
ATTATTATTT TTTAGATATT GTATAACTCT TGTTTTATTT TTAATTTTGT TACTATTCA 300
AAGGCATTTG TTTGTAGTGT TATTTTCGAGT AGGTTTTATG GGTGAACAAC CCTTGACCCG 360
CAAATCAATC ACAAGAGTTC AACATTTTAT TTATTTTGAA ATGTATTAAA AATCGTTAAT 420
CTATATATTC GCCCCATTAT TGGGATTAAA TATTCACAAG GGTTAGACC GTCATGAGAC 480
AGATTAGTTT TATCTTACTG ATGGTCACAT CACAATAGTA ATTCAACTTA ATACGAGAGG 540
AACCATTGAT TCACGCAATT GGTCAATCGCA CTTAGTTGAA AAGCTAGGGG TCGGAAGCTA 600
CCGTACGCTG GATTATGATT GAACACCTCT AAGTCAGAAAT CCGAATTAGA AACAAATGCAC 660
GTGTCCGTTG CCTGATTGCC AACCCCAATA ACACGTGTTG TAGGTTTAAAC CATGTTTATG 720
AAAGATAAGG TTTTTTTTTT TATAAGCAAG CAACTATAGG GGTTTACTTC CGTGCGCAA 780
TTTTTTAGGT ACCTATTTTG GGAGGGGGGA TTATGATTCA AGTGAAGAA AGTTGGCACA 840
CACACAATCA GTACATCTGT TTTGACAGAG ACACAGCCTA AAAACAGCAG CAAACAAGCC 900
TAAAGGAATC ACCCAAAAAC AACAAACAAA AGTACAGAGG AAAACAAGA AATCCCTGTT 960
ACCACCAAGC TGAATAAAAG AAAATAAAAC TCAACTTTTG GCAATAAAA CCTCCTACC 1020
CTCAACCCCT AACACGCAA CAATCAGCAA TACTCCAAGC AACCATTTTC CTTACAAGTT 1080

FIGURE 7A



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TGTTTTTCTT GTGATTAAATC CAT ATG GCT AGC TCC ATG TCC CTT AAG CTT GCA 1133
Met Ala Ser Ser Met Ser Leu Lys Leu Ala>

TGT CTG CTA GTG TTG TGC ATG GTG GTG GGT GCA CCC CTG GCT CAA GGG 1181
Cys Leu Leu Val Leu Cys Met Val Val Gly Ala Pro Leu Ala Gln Gly>

GAC GTA ACC CGT GCT GAT GGC GTA GTC ACC CTT CCA CGC TGC CTT CCT 1229
Asp Val Thr Arg Ala Asp Gly Val Val Thr Leu Pro Arg Cys Leu Pro>

TTA TTG ATA GGG AAT GGT AAT GGT GCT GAT GCT GAT GAT GCC CCA 1277
Leu Leu Ile Gly Asn Gly Asn Gly Ala Asp Val Asp Ala Pro>

GCT TGC TGC GAC ATC AGG GGT CTC TTG AGC TCG CTG CTC TGT GGT 1325
Ala Cys Cys Asp Ile Val Arg Gly Leu Leu Ser Ser Leu Cys Gly>

GGT GTT TAGGAACCG ATCTAGCTTG AAATCGGGTT CGGATACGGG TGGAGTTTCA 1380
Gly Val>

AATTGGTGTG TTATGGAATC CCAACTTAAT CGTGTTTAGG GGTGGGATCC AATTGTGTGA 1440

TACATTACAG AGCATGGTTG TGGATTGTTT TCTCATATGT TTTGATTGAC TTGCTTGATA 1500

CATTGGAATGA TTCGATAAGG TGACCGGTTT ACCTGGGTAT CCAACCATCA TCCGATTACT 1560

TTTTAATAAT TATTTGTTTC TTCTTTATGT TGTCTGTCTT TTTGTTTCTT GATCTATAAC 1620

ATTATATTG CCCAAATTTT CGCATTTTCC ATATGTAGCT TATATATGTA TATATATATT 1680

CAATAAAGTA TATTGATTTA GCAGATGATT TGTGTATATA TTAAATCAA ATCAAACATT 1740

AATGATCATT CACTAGCGTC TTAATCTTGA AAAATTCATC AACGGTTATC CTTTGCAGCA 1800

TATATAAAAA AAATTGCCAA CCCTATGCTT TTACACCTAA TTCAAGGGAT AACATAAGTC 1860

GATTAAACG A 1871

FIGURE 7B



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Coker 130	Yxy, Y	Yxy, x	Yxy, Y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
1	80.35	.3206	.3266	91.84	0.16	5.51	91.84	5.51	88.4
2	77.62	.3232	0.3282	90.6	0.66	6.45	90.6	6.48	84.2
3	80.98	.3197	0.3257	92.12	0.13	5.04	92.12	5.04	88.6
4	80.16	.3200	0.3255	91.75	0.35	5.00	91.75	5.01	86.1
5	77.03	.3220	0.3271	90.33	0.61	5.84	90.33	5.87	84.1
6	73.67	.3258	0.3293	88.76	1.35	7.14	88.76	7.26	79.4
7	82.43	.3178	0.3237	92.76	0.15	4.05	92.76	4.05	87.9
8	82.21	.3196	0.3255	92.66	0.19	4.99	92.66	4.99	87.9
9	81.19	.3194	0.3241	92.21	0.77	4.42	92.21	4.48	80.2
10	76.11	.3243	0.329	89.9	0.74	6.89	89.9	6.92	84
11	82.28	.3178	0.3236	92.69	0.19	4.00	92.69	4.00	87.3
TOTAL	874.03	3.5302	3.5883	1005.62	5.30	59.33	1005.62	59.61	938.10
MEAN	79.46	.3209	.3262	91.42	0.48	5.39	91.42	5.42	85.28
S.D.	2.91	.0026	.0020	1.33	0.38	1.08	1.33	1.11	3.22
RANGE	82.43-73.67	.3858-.3178	0.3293-.3236	92.76-88.76	1.35-.13	7.14-4.00	92.76-88.76	7.26-4.00	88.6-79.4
AVER DEV	2.44	.0021	.0017	1.11	0.31	0.88	1.11	0.90	2.64
Coker 130	Hunter L	Hunter a	Hunter B						
1	89.63	0.15	5.42						
2	88.10	0.66	6.27						
3	89.98	0.13	4.98						
4	89.53	0.36	4.94						
5	87.76	0.61	5.69						
6	85.83	1.35	6.85						
7	90.79	0.15	4.03						
8	90.67	0.19	4.95						
9	90.10	0.78	4.38						
10	87.23	0.75	6.65						
11	90.70	0.19	3.98						
TOTAL	980.32	5.32	58.14						
MEAN	89.12	0.48	5.29						
S.D.	1.65	0.39	0.99						
RANGE	90.79-85.83	1.35-.13	6.85-3.98						
AVER DEV	1.37	0.31	0.81						

FIGURE 9



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5148	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
68-1	60.76	0.34	0.35	82.24	2.32	15.11	82.24	15.28	81.3
68-1	61.89	0.34	0.34	82.82	1.97	14.31	82.85	14.44	82.2
50-2-1	78.39	0.3324	0.3375	90.95	0.68	11.29	90.95	11.31	86.6
50-2-1									
(lint fiber)	21.49	.3155	0.3489	53.48	-8.01	7.97	53.48	11.29	135.2
5148	Hunter L	Hunter a	Hunter B						
68-1	77.94	2.25	13.35						
68-1	78.67	1.92	12.75						
50-2-1	88.53	0.69	10.71						
50-2-1									
(lint fiber)	46.35	-6.35	6.06						

FIGURE 10



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5149	Yxy, Y	Yxy, x	Yxy, Y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
68-1	65.75	0.3351	0.34	84.86	0.72	11.9	84.86	11.92	86.6
68-1	62.54	0.3458	0.3474	83.19	2.14	15.84	83.19	15.98	82.4
68-1	62.56	0.3458	0.3474	83.2	2.14	15.85	83.2	15.99	82.4
8-1	84.72	0.3196	0.3278	93.76	0.89	5.87	93.76	5.93	98.6
68-1	64.97	0.3316	0.3354	84.46	1.17	9.81	84.46	9.87	83.3
17-2	64.42	0.3423	0.3436	84.18	2.26	14.19	84.18	14.36	81
17-3	60.97	0.3475	0.3475	82.36	2.74	16.03	82.36	16.26	80.4
17-15-1	64.02	0.3433	0.3444	83.97	2.34	14.57	83.97	14.75	80.9
21-1	59.32	0.3443	0.3445	81.46	2.64	14.41	81.46	14.64	79.7
21-3	63.64	0.34	0.3409	83.77	2.4	12.89	83.77	13.11	79.5
21-6	67.12	0.3372	0.3394	85.56	1.88	12.15	85.56	12.29	81.3
50-3-1	61.26	0.3502	0.3511	82.51	2.4	17.63	82.51	17.79	82.3
67-1	64.34	0.3434	0.3442	84.13	2.48	14.58	84.13	14.78	80.4
68-1	64.12	0.3442	0.3447	84.02	2.58	14.85	84.02	15.07	80.2
68-2	70.21	0.3428	0.3447	87.09	2.05	15.04	87.09	15.17	82.3
68-3	63.81	0.3457	0.3468	83.86	2.35	15.76	83.86	15.93	81.6
5149	Hunter L	Hunter a	Hunter B						
68-1	81.08	0.71	10.89						
68-1	79.08	2.08	14						
68-1	79.09	2.09	14.02						
8-1	92.04	0.91	5.81						
68-1	80.6	1.15	9.06						
17-2	80.25	2.21	12.75						
17-3	78.08	2.68	14.09						
17-15-1	80.01	2.29	13.05						
21-1	77.01	2.56	12.73						
21-3	79.77	2.35	11.65						
21-6	81.92	1.86	11.14						
50-3-1	78.26	2.33	15.36						
67-1	80.2	2.43	13.07						
68-1	80.07	2.53	13.28						
68-2	83.79	2.04	13.68						
68-3	79.87	2.3	14						

FIGURE 11



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5616	Yxy, Y	Yxy, x	Yxy, Y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
11-1	72.26	0.3215	0.3254	88.09	1.1	5.06	88.09	5.17	77.8
11-2	58.69	0.3284	0.3335	81.12	0.6	8.36	81.12	8.38	85.9
11-2	52.78	0.3358	0.3335	77.74	3.55	9.22	77.74	9.87	69
11-1	72.03	0.3312	0.3338	87.98	1.72	9.52	87.98	9.67	79.8
11-1	72.34	0.3295	0.332	88.13	1.79	8.64	88.13	8.82	78.4
11-1	71.98	0.3295	0.3313	87.95	2.09	8.39	87.95	8.64	76.1
11-1	73.01	0.3256	0.3305	88.45	0.68	7.51	88.45	7.54	84.9
17-1-2	75.85	0.3274	0.3306	89.78	1.52	7.94	89.78	8.08	79.3
17-3-1	72.6	0.3271	0.3303	88.25	1.48	7.66	88.25	7.8	79.1
17-4-1	69.02	0.3352	0.3377	86.51	1.78	11.37	86.51	11.5	81.2
25-11-1	69.5	0.3364	0.3401	86.75	1.26	12.41	86.75	12.47	84.2
25-28-1	72.21	0.3324	0.3343	88.06	2.09	9.9	88.06	10.11	78.2
25-36-2	70.46	0.3327	0.3353	87.22	1.73	10.22	87.22	10.36	80.5
35-35-1	75.59	0.3268	0.3299	89.66	1.56	7.58	89.66	7.73	78.4
50-12-1	73.13	0.3284	0.3316	88.5	1.46	8.36	88.5	8.48	80.1
KS-11-2	65.33	0.3371	0.3388	84.65	2.07	11.83	84.65	12	80.1
5616	Hunter L	Hunter a	Hunter B						
11-1	85	1.09	4.89						
11-2	76.61	0.58	7.64						
11-2	72.64	3.38	8.22						
11-1	84.87	1.72	8.97						
11-1	85.05	1.79	8.2						
11-1	84.84	2.08	7.96						
11-1	85.44	0.67	7.18						
17-1-2	87.08	1.52	7.62						
17-3-1	85.2	1.48	7.31						
17-4-1	83.07	1.76	10.52						
25-11-1	83.36	1.25	11.43						
25-28-1	84.97	2.08	9.32						
25-36-2	83.94	1.72	9.56						
35-35-1	86.94	1.57	7.29						
50-12-1	85.51	1.46	7.96						
KS-11-2	80.82	2.04	10.81						

FIGURE 12



BC	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
12 Green	33.34	0.3779	0.3717	66.01	4.24	24.18	66.01	24.54	80.1
22 Brown	38.18	0.3778	0.3662	68.15	6.18	23.31	68.15	24.11	75.2
3 Red	24.23	0.4055	0.3728	56.31	10.96	25.52	56.31	27.77	66.9
4 Ivory	46.84	0.3657	0.3599	74.08	4.6	21.13	74.08	21.62	77.8
BC	Hunter L	Hunter a	Hunter B						
12 Green	59.44	3.79	17.92						
22 Brown	61.78	5.62	17.69						
3 Red	49.22	9.42	17.14						
4 Ivory	68.43	4.31	17.02						

FIGURE 13